ABSTRACT OF THE DISCLOSURE

The present invention relates to a method of predicting the evolutionary potential of a mutant resistance gene, which is carried out by providing a host cell which includes a mutant resistance gene either including two or more nucleic acid modifications or encoding a mutant polypeptide including two or more amino acid modifications, wherein the mutant resistance gene or mutant polypeptide confers a selectable advantage to the host cell, and then determining whether the mutant resistance gene is likely to evolve through two or more independent mutation events. Also disclosed are the resulting mutant resistance genes and their encoded polypeptides, and methods of using such mutant resistance genes to screen a drug for anti-pathogenic activity against a pathogen and assessing the potential longevity of a candidate anti-pathogenic drug.